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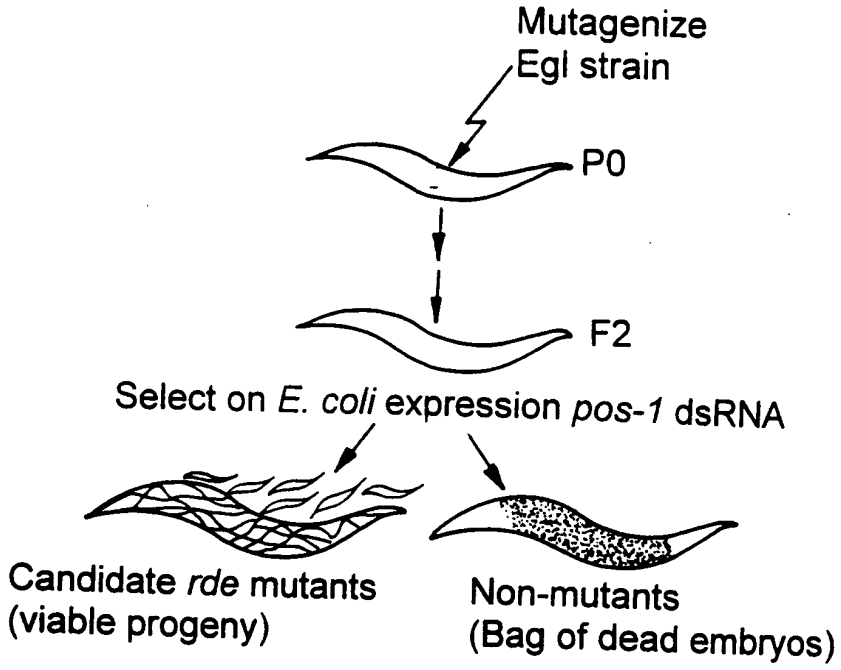

FIG. 1A

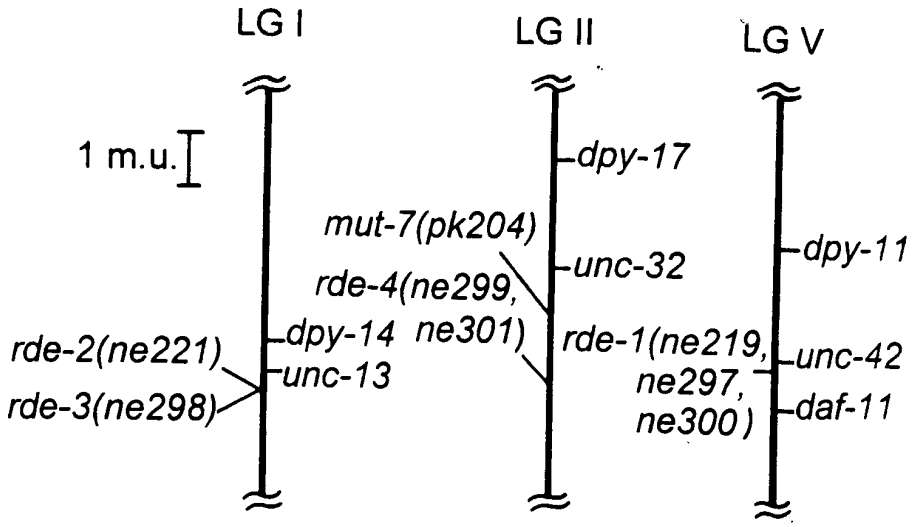

FIG. 1B

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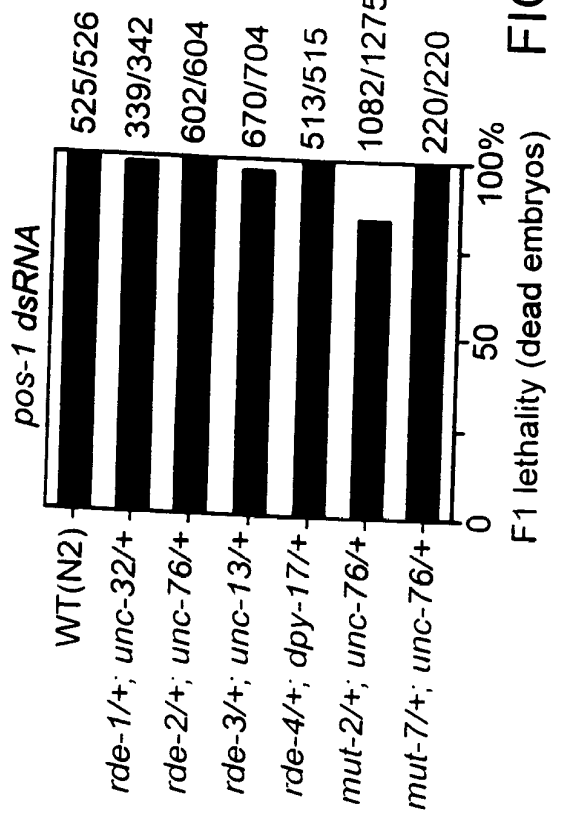

FIG. 2A

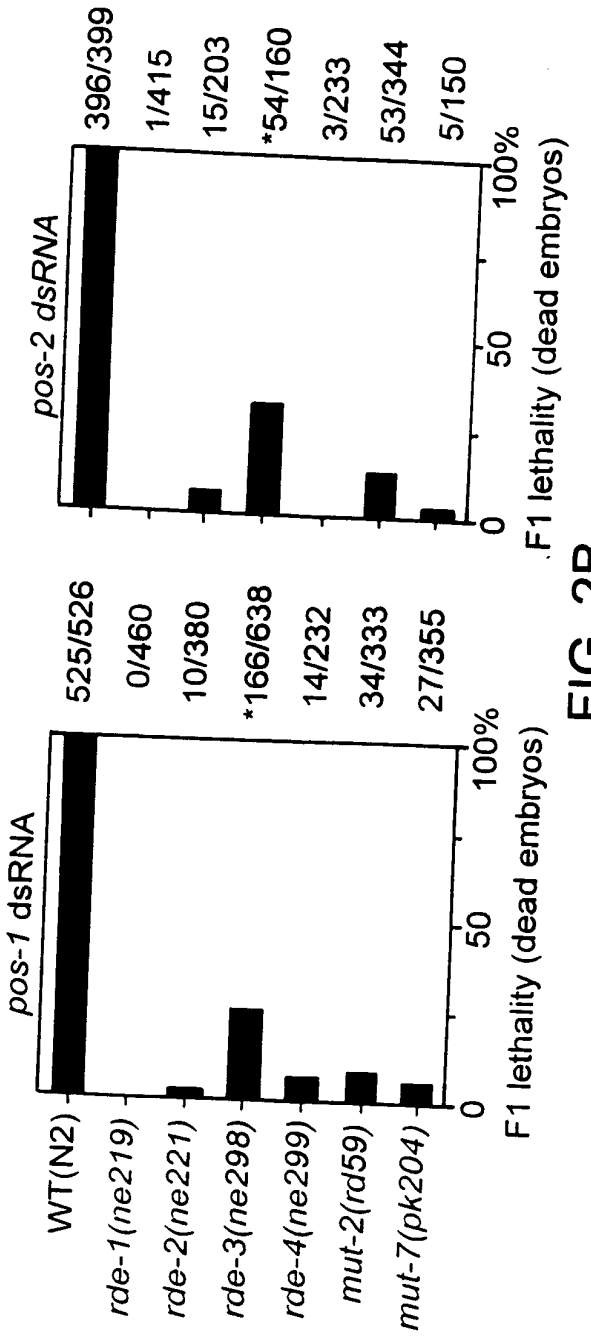

FIG. 2B

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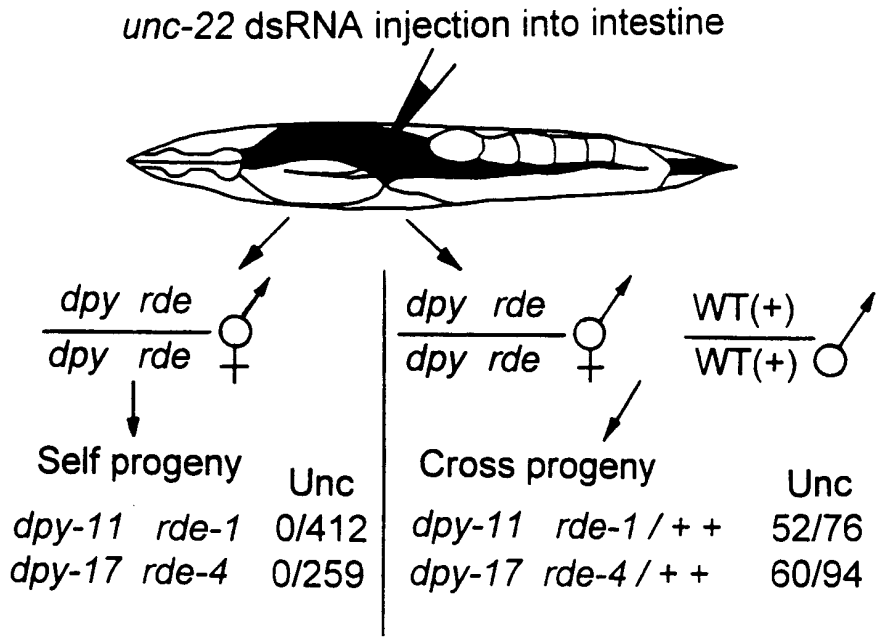

FIG. 3

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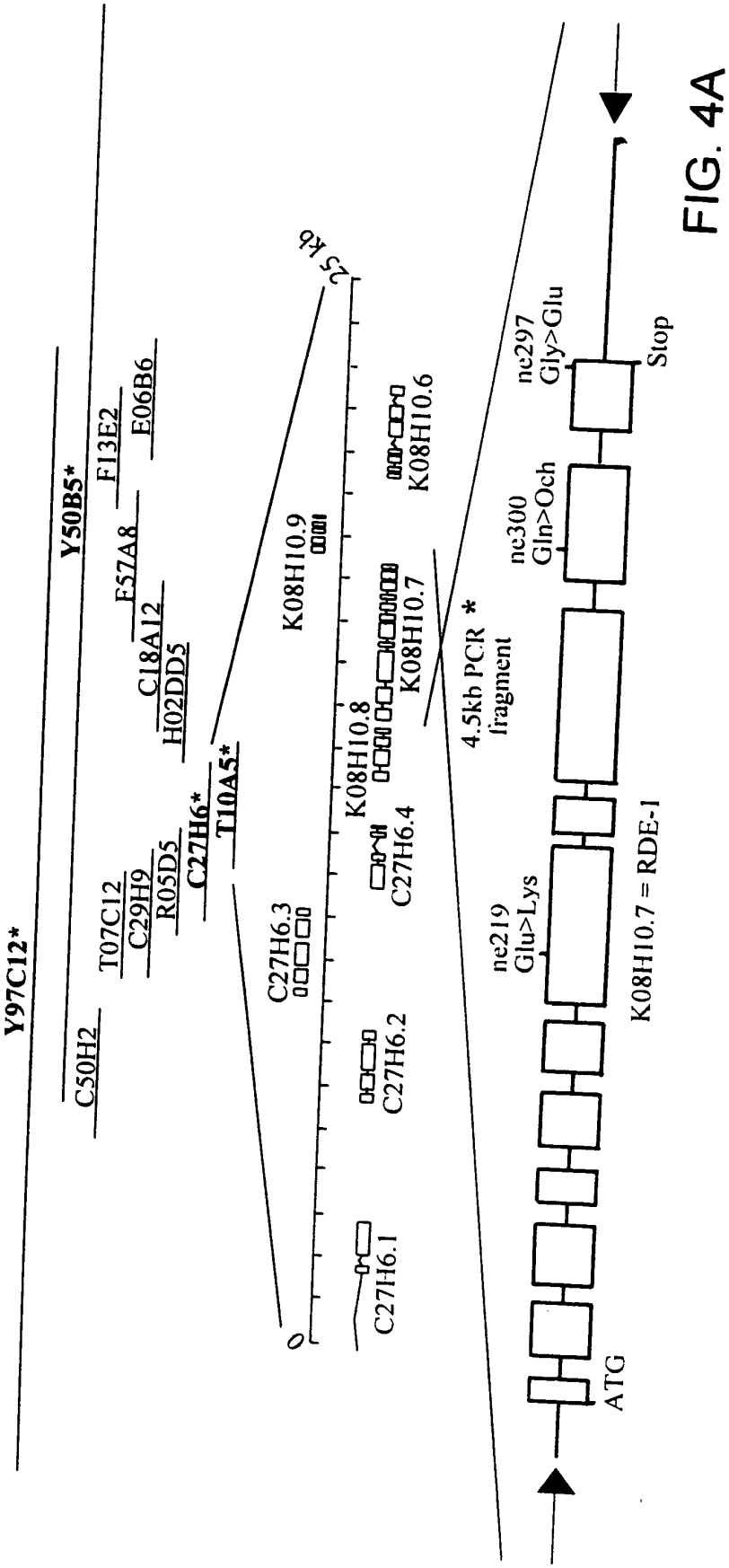

FIG. 4A

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FIG. 4B-1

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FIG. 4B-2

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FIG. 4B-3

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cagtcacaaagtgatgaaacatgtcctcgaatttcccgaattggaaaaaggatttatcgtcattctctcgatccggta

tgatcaattattagcagctataagatatataattataggagatgaaatggcttgcgaggcccactg

gtaaatgcgacggcaaattctatgagaagaaagtacttctttggtaaattggttcaagttcctccagcaaaatttacgat

cgggaatactacgagtatgaagtgaaaatgacaaaggaagtattgaatagaaaaccaggaaaaccttcccaaaaaag

agaaattccaatgtaagtgcttgtaaattagtcaaaactaatttatttttcagtcccgatcgtgcaaaactcttctggc

aacatcttcggcatgagaagaagcagacagatttattctcgaagactatgttttgatgaaaaggacactgtttatagt

gttgtcgactgaacactgtcacatcaaaaatgctggtttcggagaaagtagtaaaaaaaggattcggagaaaaaagatg

aaaggatttggagaaaaaaatcttatacacaatgatacttacctatcgtaaaaaatttcacctgaacttttagtcgagaaa

atccggaaaaagacgaagaagcgaatcggagttacaaatttcctgaaggtttatgaaaaacacgcattataacaaacaa

ttagctttcagaatgttatgacccagaaagttcgctacgcgcgcctttgtgaacgaggagattaaagtgtgagttgcaata

atataataataatcacctcaactcatttatatttaagacaattcgcgaaaaaatttgtgtacgataataattcaat

FIG. 5A

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tctgcgagttcctgaatcgtttcacgatccaaacagattcgaacaatcattagaagtagcaccaagaatcgaagcatggt

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taaaaaatcatgtgatttttgttgaagttgtcgataaactattctacaatgcaccgaaaatgtctcttctggattatctt

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aaatgttagtttaaattattcaaacaattaatatacaaattgattttcaggtcgagattgacagaacgacatctgacatt

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ggtgatgcaagacaagtttctaaagcgagctacacgaaaacctcacgactacaaagaaaataccctaaaaatgctgaaa

aattggatttctcttctgaagagctaaattttgttgaaagatttggattatgctccaaacttcagatgatcgaatgtcca

ggaaaggttttgaaagagccaatgcttgtgaatagtgtaaatgaacaaattaaaatgacaccagtgattcgtggatttca

agaaaaacaattgaatgtggttcccgaaaaagaactttgctgtgctgtttttgtagtcaacgaaacagcgggaaatccat

gcttagaagagaacgacgttgtgtaagtgttttctacgtagattattccgaaatattttcagtaagttctacaccgaact

aattggtggttgcaagttccgtggaatacgaattggtgccaatgaaaacagaggagcgcaatctattatgtacgacgcga

cgaaaaatgaatatgccgtaagtttcagaaaattgaaagtttttaaatatcatatttacagttctacaaaaattgtacac

taaataccggaatcggtagatttgaaatagccgcaacagaagcgaagaatatgtttgaacgtcttcccgataaagaaca

aaagtcttaatgttcattatcatttccaaacgacaactgaatgcttacggttttgtgaaacattattgcgatcacaccat

cggtgtagctaatcagcatattacttctgaaacagtcacaaaagctttggcatcactaaggcacgagaaaggatcaaaac

gaattttctatcaaattgcattgaaaatcaacgcgaaattaggaggtattaccaggagcttgactggtcagaaattgca

gaaatatcaccagaagaaaaagaaagacggaaaacaatgccattaactatgtatgttggaattgatgtaactcatccaa

ctcctacagtggaattgattattctatagcggctgtagtagcgagtatcaatccaggtggaactatctatcgaaatatga

ttgtgactcaagaagaatgtcgtcccggtgagcgtgcagtggctcatggacgggaaagaacagatattttggaagcaaa

ttcgtgaaattgctcagagaattcgcagaagtgagttgtcttgagtatttaaaagatctctgggatttttaatttttttg

FIG. 5B

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taaacttcagaacaacgacaatcgagcaccagcgcatattgtagtctatcgagacggagttagcgattcggagatgcta

cgtgttagtcatgatgagcttcgatctttaaaaagcgaagtaaaacaattcatgtcggaacgggatggagaagatccaga

gccgaagtacacgttcattgtgattcagaaaagacacaatacacgattgcttcgaagaatggaaaaagataagccagtg

tcaataaagatcttactcctgctgaaacagatgtcgctgttgctgctgttaaacaatgggaggaggatatgaaagaaagc

aaagaaactggaattgtgaacccatcatccggaacaactgtggataaacttatcgtttcgaaatacaaattcgatttttt

ctggcatctcatcatggtgtcctggtacatctcgtccaggacattacactgttatgtatgacgataaaggaatgagcc

agatgaagtctatgtaagcgttttgaatagcagttagcgatttttaggatttgtaatccgcatatagttattataaaaa

aatgtttcagaaaatgacctacggacttgctttctctctgctagatgtcgaaaacccatctcgttgcctgttccggttc

attatgctcatttatcatgtgaaaaagcgaaagagcttatcgaacttacaaggaacattacatcggtgactatgcacag

ccacggactcgacacgaaatggaacatttctccaaactaacgtgaagtaccctggaatgtcgttcgcataacatttgc

aaaagtgtcgcccgtttcaatcaaatttttcaattgtagatattgtacttactttttttttaaagccccggtttcaaaaatt

catccatgactaacgtttcataaattactgaaattt (SEQ ID NO:1)

FIG. 5C

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CAGCCACAAAGTGATGAAAC- 3' UTR

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1/1                                                    31/11
ATG TCC TCG AAT TTT CCC GAA TTG GAA AAA GGA TTT TAT CGT CAT TCT CTC GAT CCG GAG
Met ser ser asn phe pro glu leu glu lys gly phe tyr arg his ser leu asp pro glu

61/21                                                  91/31
ATG AAA TGG CTT GCG AGG CCC ACT GGT AAA TGC GAC GGC AAA TTC TAT GAG AAG AAA GTA
met lys trp leu ala arg pro thr gly lys cys asp gly lys phe tyr glu lys lys val

121/41                                                 151/51
CTT CTT TTG GTA AAT TGG TTC AAG TTC TCC AGC AAA ATT TAC GAT CGG GAA TAC TAC GAG
leu leu leu val asn trp phe lys phe ser ser lys ile tyr asp arg glu tyr tyr glu

181/61                                                 211/71
TAT GAA GTG AAA ATG ACA AAG GAA GTA TTG AAT AGA AAA CCA GGA AAA CCT TTC CCA AAA
tyr glu val lys met thr lys glu val leu asn arg lys pro gly lys pro phe pro lys

241/81                                                 271/91
AAG ACA GAA ATT CCA ATT CCC GAT CGT GCA AAA CTC TTC TGG CAA CAT CTT CGG CAT GAG
lys thr glu ile pro ile pro asp arg ala lys leu phe trp gln his leu arg his glu

301/101                                                331/111
AAG AAG CAG ACA GAT TTT ATT CTC GAA GAC TAT GTT TTT GAT GAA AAG GAC ACT GTT TAT
lys lys gln thr asp phe ile leu glu asp tyr val phe asp glu lys asp thr val tyr

361/121                                                391/131
AGT GTT TGT CGA CTG AAC ACT GTC ACA TCA AAA ATG CTG GTT TCG GAG AAA GTA GTA AAA
ser val cys arg leu asn thr val thr ser lys met leu val ser glu lys val val lys

421/141                                                451/151
AAG GAT TCG GAG AAA AAA GAT GAA AAG GAT TTG GAG AAA AAA ATC TTA TAC ACA ATG ATA
lys asp ser glu lys lys asp glu lys asp leu glu lys lys ile leu tyr thr met ile

481/161                                                511/171
CTT ACC TAT CGT AAA AAA TTT CAC CTG AAC TTT AGT CGA GAA AAT CCG GAA AAA GAC GAA
leu thr tyr arg lys lys phe his leu asn phe ser arg glu asn pro glu lys asp glu

541/181                                                571/191
GAA GCG AAT CGG AGT TAC AAA TTC CTG AAG AAT GTT ATG ACC CAG AAA GTT CGC TAC GCG
glu ala asn arg ser tyr lys phe leu lys asn val met thr gln lys val arg tyr ala

601/201                                                631/211
CCT TTT GTG AAC GAG GAG ATT AAA GTA CAA TTC GCG AAA AAT TTT GTG TAC GAT AAT AAT
pro phe val asn glu glu ile lys val gln phe ala lys asn phe val tyr asp asn asn

661/221                                                691/231
TCA ATT CTG CGA GTT CCT GAA TCG TTT GAC GAT CCA AAC AGA TTC GAA CAA TCA TTA GAA
ser ile leu arg val pro glu ser phe his asp pro asn arg phe glu gln ser leu glu

721/241                                                751/251
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FIG. 6A

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GTA GCA CCA AGA ATC GAA GCA TGG TTT GGA ATT TAC ATT GGA ATC AAA GAA TTG TTC GAT
val ala pro arg ile glu ala trp phe gly ile tyr ile gly ile lys glu leu phe asp

781/261
GGT GAA CCT GTG CTC AAT TTT GCA ATT GTC GAT AAA CTA TTC TAC AAT GCA CCG AAA ATG
gly glu pro val leu asn phe ala ile val asp lys leu phe tyr asn ala pro lys met

811/271
841/281
TCT CTT CTG GAT TAT CTT CTC CTA ATT GTC GAC CCC CAG TCG TGT AAC GAT GAT GTA CGA
ser leu leu asp tyr leu leu leu ile val asp pro gln ser cys asn asp asp val arg

871/291
901/301
AAA GAT CTT AAA ACA AAA CTG ATG GCG GGA AAA ATG ACA ATC AGA CAA GCC GCG CGG CCA
lys asp leu lys thr lys leu met ala gly lys met thr ile arg gln ala ala arg pro

931/311
961/321
AGA ATT CGA CAA TTA TTG GAA AAT TTG AAG CTG AAA TGC GCA GAA GTT TGG GAT AAC GAA
arg ile arg gln leu leu glu asn leu lys leu lys cys ala glu val trp asp asn glu

991/331
1021/341
ATG TCG AGA TTG ACA GAA CGA CAT CTG ACA TTT CTA GAT TTG TGC GAG GAA AAC TCT CTT
met ser arg leu thr glu arg his leu thr phe leu asp leu cys glu glu asn ser leu

1051/351
1081/361
GTT TAT AAA GTC ACT GGT AAA TCG GAC AGA GGA AGA AAT GCA AAA AAG TAC GAT ACT ACA
val tyr lys val thr gly lys ser asp arg gly arg asn ala lys lys tyr asp thr thr

1111/371
1141/381
TTG TTC AAA ATC TAT GAG GAA AAC AAA AAG TTC ATT GAG TTT CCC CAC CTA CCA CTA GTC
leu phe lys ile tyr glu glu asn lys lys phe ile glu phe pro his leu pro leu val

1171/391
1201/401
AAA GTT AAA AGT GGA GCA AAA GAA TAC GCT GTA CCA ATG GAA CAT CTT GAA GTT CAT GAG
lys val lys ser gly ala lys glu tyr ala val pro met glu his leu glu val his glu

1231/411
1261/421
AAG CCA CAA AGA TAC AAG AAT CGA ATT GAT CTG GTG ATG CAA GAC AAG TTT CTA AAG CGA
lys pro gln arg tyr lys asn arg ile asp leu val met gln asp lys phe leu lys arg

1291/431
1321/441
GCT ACA CGA AAA CCT CAC GAC TAC AAA GAA AAT ACC CTA AAA ATG CTG AAA GAA TTG GAT
ala thr arg lys pro his asp tyr lys glu asn thr leu lys met leu lys glu leu asp

1351/451
1381/461
TTC TCT TCT GAA GAG CTA AAT TTT GTT GAA AGA TTT GGA TTA TGC TCC AAA CTT CAG ATG
phe ser ser glu glu leu asn phe val glu arg phe gly leu cys ser lys leu gln met

1411/471
1441/481
ATC GAA TGT CCA GGA AAG GTT TTG AAA GAG CCA ATG CTT GTG AAT AGT GTA AAT GAA CAA
ile glu cys pro gly lys val leu lys glu pro met leu val asn ser val asn glu gln

1471/491
1501/501
ATT AAA ATG ACA CCA GTG ATT CGT GGA TTT CAA GAA AAA CAA TTG AAT GTG GTT CCC GAA
ile lys met thr pro val ile arg gly phe gln glu lys gln leu asn val val pro glu

1531/511

FIG. 6B

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1561/521
AAA GAA CTT TGC TGT GCT GTT TTT GTA GTC AAC GAA ACA GCG GGA AAT CCA TGC TTA GAA
lys glu leu cys cys ala val phe val val asn glu thr ala gly asn pro cys leu glu

1621/541
GAG AAC GAC GTT GTT AAG TTC TAC ACC GAA CTA ATT GGT GGT TGC AAG TTC CGT GGA ATA
glu asn asp val val lys phe tyr thr glu leu ile gly gly cys lys phe arg gly ile

1681/561
CGA ATT GGT GCC AAT GAA AAC AGA GGA GCG CAA TCT ATT ATG TAC GAC GCG ACG AAA AAT
arg ile gly ala asn glu asn arg gly ala gln ser ile met tyr asp ala thr lys asn

1741/581
GAA TAT GCC TTC TAC AAA AAT TGT ACA CTA AAT ACC GGA ATC GGT AGA TTT GAA ATA GCC
glu tyr ala phe tyr lys asn cys thr leu asn thr gly ile gly arg phe glu ile ala

1801/601
GCA ACA GAA GCG AAG AAT ATG TTT GAA CGT CTT CCC GAT AAA GAA CAA AAA GTC TTA ATG
ala thr glu ala lys asn met phe glu arg leu pro asp lys glu gln lys val leu met

1861/621
TTC ATT ATC ATT TCC AAA TCA CAA CTG AAT GCT TAC GGT TTT GTG AAA CAT TAT TGC GAT
phe ile ile ile ser lys arg gln leu asn ala tyr gly phe val lys his tyr cys asp

1921/641
CAC ACC ATC GGT GTA GCT AAT CAG CAT ATT ACT TCT GAA ACA GTC ACA AAA GCT TTG GCA
his thr ile gly val ala asn gln his ile thr ser glu thr val thr lys ala leu ala

1981/661
TCA CTA AGG CAC GAG AAA GGA TCA AAA CGA ATT TTC TAT CAA ATT GCA TTG AAA ATC AAC
ser leu arg his glu lys gly ser lys arg ile phe tyr gln ile ala leu lys ile asn

2041/681
GCG AAA TTA GGA GGT ATT AAC CAG GAG CTT GAC TGG TCA GAA ATT GCA GAA ATA TCA CCA
ala lys leu gly gly ile asn gln glu leu asp trp ser glu ile ala glu ile ser pro

2101/701
GAA GAA AAA GAA AGA CGG AAA ACA ATG CCA TTA ACT ATG TAT GTT GGA ATT GAT GTA ACT
glu glu lys glu arg arg lys thr met pro leu thr met tyr val gly ile asp val thr

2161/721
CAT CCA ACC TCC TAC AGT GGA ATT GAT TAT TCT ATA GCG GCT GTA GTA GCG AGT ATC AAT
his pro thr ser tyr ser gly ile asp tyr ser ile ala ala val val ala ser ile asn

2221/741
CCA GGT GGA ACT ATC TAT CGA AAT ATG ATT GTG ACT CAA GAA GAA TGT CGT CCC GGT CAG
pro gly gly thr ile tyr arg asn met ile val thr gln glu glu cys arg pro gly glu

2281/761
CGT GCA GTG GCT CAT GGA CGG GAA AGA ACA GAT ATT TTG GAA GCA AAG TTC GTG AAA TTG
arg ala val ala his gly arg glu arg thr asp ile leu glu ala lys phe val lys leu

2341/781
CTC AGA GAA TTC GCA GAA AAC AAC GAC AAT CGA GCA CCA GCG CAT ATT GTA GTC TAT CGA
leu arg glu phe ala glu asn asn asp asn arg ala pro ala his ile val val tyr arg

FIG. 6C

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2401/801
GAC GGA GTT AGC GAT TCG GAG ATG CTA CGT 2431/811
asp gly val ser asp ser glu met leu arg GTT AGT CAT GAT GAG CTT CGA TCT TTA AAA val ser his asp glu leu arg ser leu lys

2461/821
AGC GAA GTA AAA CAA TTC ATG TCG GAA CGG 2491/831
ser glu val lys gln phe met ser glu arg GAT GGA GAA GAT CCA GAG CCG AAG TAC ACG asp gly glu asp pro glu pro lys tyr thr

2521/841
TTC ATT GTG ATT CAG AAA AGA CAC AAT ACA 2551/851
phe ile val ile gln lys arg his asn thr CGA TTG CTT CGA AGA ATG GAA AAA GAT AAG arg leu leu arg arg met glu lys asp lys

2581/861
CCA GTG GTC AAT AAA GAT CTT ACT CCT GCT 2611/871
pro val val asn lys asp leu thr pro ala GAA ACA GAT GTC GCT GTT GCT GCT GTT AAA glu thr asp val ala val ala ala val lys

2641/881
CAA TGG GAG GAG GAT ATG AAA GAA AGC AAA 2671/891
gln trp glu glu asp met lys glu ser lys GAA ACT GGA ATT GTG AAC CCA TCA TCC GGA glu thr gly ile val asn pro ser ser gly

2701/901
ACA ACT GTG GAT AAA CTT ATC GTT TCG AAA 2731/911
thr thr val asp lys leu ile val ser lys TAC AAA TTC GAT TTT TTC TTG GCA TCT CAT tyr lys phe asp phe phe leu ala ser his

2761/921
CAT GGT GTC CTT GGT ACA TCT CGT CCA GGA 2791/931
his gly val leu gly thr ser arg pro gly CAT TAC ACT GTT ATG TAT GAC GAT AAA GGA his tyr thr val met tyr asp asp lys gly

2821/941
ATG AGC CAA GAT GAA GTC TAT AAA ATG ACC 2851/951
met ser gln asp glu val tyr lys met thr TAC GGA CTT GCT TTT CTC TCT GCT AGA TGT tyr gly leu ala phe leu ser ala arg cys

2881/961
CGA AAA CCC ATC TCG TTG CCT GTT CCG GTT 2911/971
arg lys pro ile ser leu pro val pro val CAT TAT GCT CAT TTA TCA TGT GAA AAA GCG his tyr ala his leu ser cys glu lys ala

2941/981
AAA GAG CTT TAT CGA ACT TAC AAG GAA CAT 2971/991
lys glu leu tyr arg thr tyr lys glu his TAC ATC GGT GAC TAT GCA CAG CCA CGG ACT tyr ile gly asp tyr ala gln pro arg thr

3001/1001
CGA CAC GAA ATG GAA CAT TTT CTC CAA ACT 3031/1011
arg his glu met glu his phe leu gln thr AAC GTG AAG TAC CCT GGA ATG TCG TTC GCA asn val lys tyr pro gly met ser phe ala

3061/1021
TAA CAT TTT GCA AAA GTG TCG CCC GTT TCA 3091/1031
OCH (SEQ ID NO:3) ATC AAA TTT TTC AAT TGT AGA TAT TGT ACT

3121/1041
TAC TTT TTT TTA AAG CCC GGT TTC AAA AAT 3151/1051
TCA TTC CAT GAC TAA CGT TTT CAT AAA TTA

3181/1061
CTT GAA ATT TAA AAA AAA AAA AAA AAA (SEQ ID NO:2)

FIG. 6D

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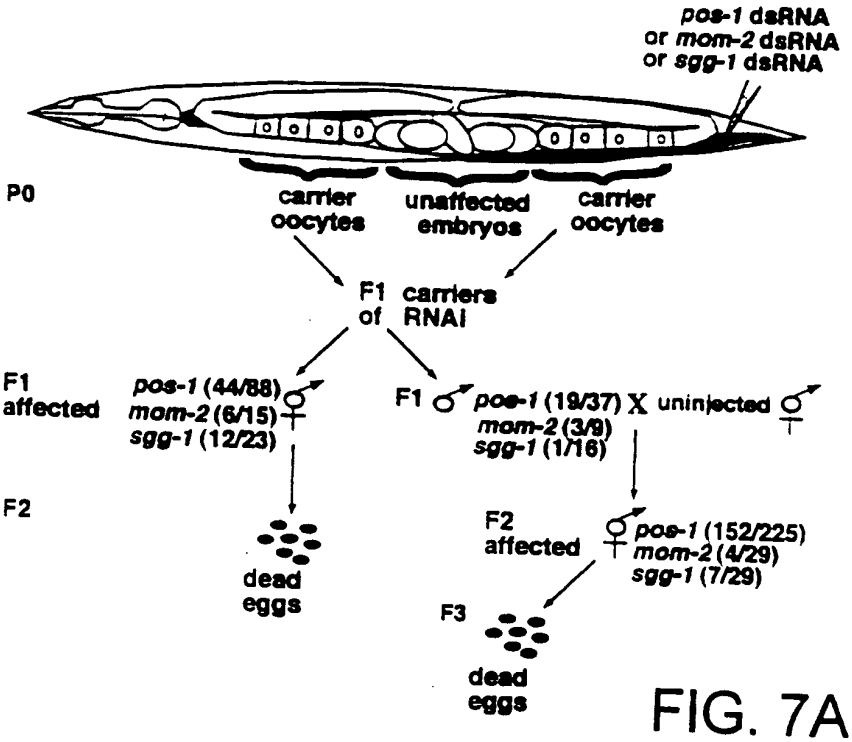

FIG. 7A

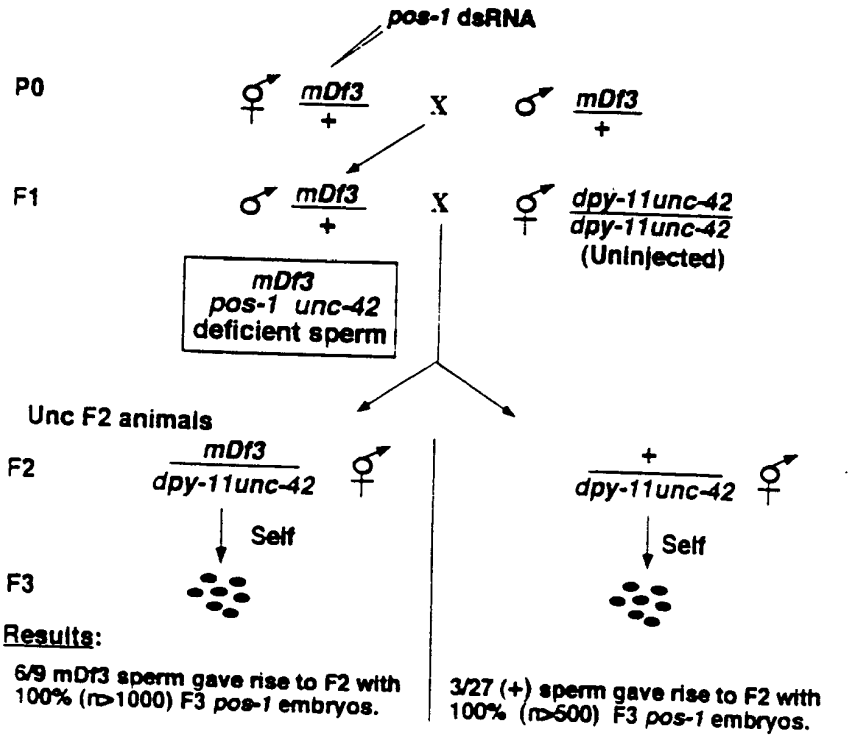

FIG. 7B

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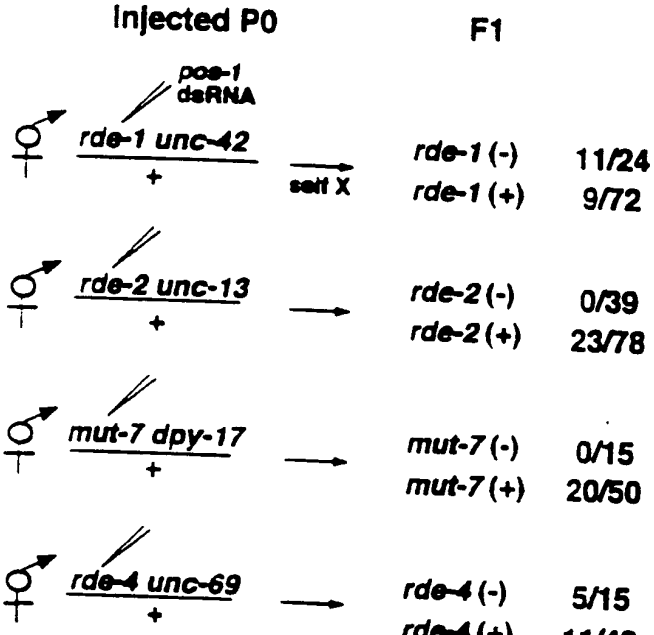

FIG. 8A

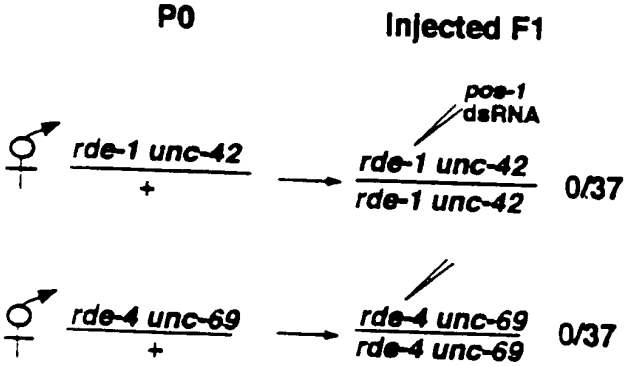

FIG. 8B

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FIG. 9A

FIG. 9B

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```
          10         20         30         40         50         60
ATGGATTTAACCAAACTAACGTTTGAAAGCGTTTTCGGTGGATCAGATGTTCCTATGAAG
M  D  L  T  K  L  T  F  E  S  V  F  G  G  S  D  V  P  M  K

          70         80         90        100        110        120
CCTTCCCGATCGGAGGATAACAAAACGCCAAGAAACAGAACAGATTTGGAGATGTTTCTG
P  S  R  S  E  D  N  K  T  P  R  N  R  T  D  L  E  M  F  L

         130        140        150        160        170        180
AAGAAAACTCCCCTCATGGTACTAGAAGAGGCTGCTAAGGCTGTCTATCAAAAGACGCCA
K  K  T  P  L  M  V  L  E  E  A  A  K  A  V  Y  Q  K  T  P

         190        200        210        220        230        240
ACTTGGGGCACTGTCGAACTTCCTGAAGGCTTCGAGATGACGTTGATTCTGAATGAAATT
T  W  G  T  V  E  L  P  E  G  F  E  M  T  L  I  L  N  E  I

         250        260        270        280        290        300
ACTGTAAAAGGCCAGGCAACAAGCAAGAAAGCTGCGAGACAAAAGGCTGCTGTTGAATAT
T  V  K  G  Q  A  T  S  K  K  A  A  R  Q  K  A  A  V  E  Y

         310        320        330        340        350        360
TTACGCAAGGTTGTGGAGAAAGGAAAGCACGAAATCTTTTTCATTCCTGGAACAACCAAA
L  R  K  V  V  E  K  G  K  H  E  I  F  F  I  P  G  T  T  K

         370        380        390        400        410        420
GAAGAAGCTCTTTCGAATATTGATCAAATATCGGATAAGGCTGAGGAATTGAAACGATCA
E  E  A  L  S  N  I  D  Q  I  S  D  K  A  E  E  L  K  R  S

         430        440        450        460        470        480
ACTTCAGATGCTGTTCAGGATAACGATAACGATGATTCGATTCCTACAAGTGCTGAATTT
T  S  D  A  V  Q  D  N  D  N  D  D  S  I  P  T  S  A  E  F

         490        500        510        520        530        540
CCACCTGGTATTTCGCCAACCGAGAATTGGGTCGGAAAGTTGCAGGAAAAATCTCAAAAA
P  P  G  I  S  P  T  E  N  W  V  G  K  L  Q  E  K  S  Q  K

         550        560        570        580        590        600
AGCAAGCTGCAAGCCCCAATCTATGAAGATTCCAAGAATGAGAGAACCGAGCGTTTCTTG
S  K  L  Q  A  P  I  Y  E  D  S  K  N  E  R  T  E  R  F  L

         610        620        630        640        650        660
GTTATATGCACGATGTGCAATCAAAAAACCAGAGGAATCAGAAGTAAGAAGAAGGACGCA
V  I  C  T  M  C  N  Q  K  T  R  G  I  R  S  K  K  K  D  A

         670        680        690        700        710        720
AAGAATCTTGCAGCATGGTTGATGTGGAAAGCGTTGGAAGACGGTATCGAATCTCTGGAA
K  N  L  A  A  W  L  M  W  K  A  L  E  D  G  I  E  S  L  E

         730        740        750        760        770        780
TCATATGATATGGTTGATGTGATTGAAAATTTGGAAGAAGCTGAACATTTACTCGAAATT
S  Y  D  M  V  D  V  I  E  N  L  E  E  A  E  H  L  L  E  I
```

FIG. 10A

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```
          790         800         810         820         830         840
CAGGATCAAGCATCCAAGATTAAAGACAAGCATTCCGCACTGATTGATATACTCTCGGAC
Q  D  Q  A  S  K  I  K  D  K  H  S  A  L  I  D  I  L  S  D

          850         860         870         880         890         900
AAGAAAAGATTTTCAGACTACAGCATGGATTTCAACGTATTATCAGTGAGCACAATGGGA
K  K  R  F  S  D  Y  S  M  D  F  N  V  L  S  V  S  T  M  G

          910         920         930         940         950         960
ATACATCAGGTGCTATTGGAAATCTCGTTCCGGCGTCTAGTTTCTCCAGACCCCGACGAT
I  H  Q  V  L  L  E  I  S  F  R  R  L  V  S  P  D  P  D  D

          970         980         990        1000        1010        1020
TTGGAAATGGGAGCAGAACACACCCAGACTGAAGAAATTATGAAGGCTACTGCCGAGAAG
L  E  M  G  A  E  H  T  Q  T  E  E  I  M  K  A  T  A  E  K

         1030        1040        1050        1060        1070        1080
GAAAAGCTACGGAAGAAGAATATGCCAGATTCCGGGCCGCTAGTGTTTGCTGGACATGGT
E  K  L  R  K  K  N  M  P  D  S  G  P  L  V  F  A  G  H  G

         1090        1100        1110        1120        1130        1140
TCATCGGCGGAAGAGGCTAAACAGTGTGCTTGTAAATCGGCGATTATCCATTTCAACACC
S  S  A  E  E  A  K  Q  C  A  C  K  S  A  I  I  H  F  N  T

         1150        1160        1170        1180        1190        1200
TATGATTTCACGGATTGAAAATATTATTGCGTATTCCTGAAAAATGAAGCGTCTGAATGA
Y  D  F  T  D  *  K  Y  Y  C  V  F  L  K  N  E  A  S  E  *

         1210        1220        1230
TTATAAAAAAAAAAAAAAAAA
L  *  K  K  K  K  K
```

(SEQ ID NO:4)
(SEQ ID NO:5)

FIG. 10B

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FIG. 11

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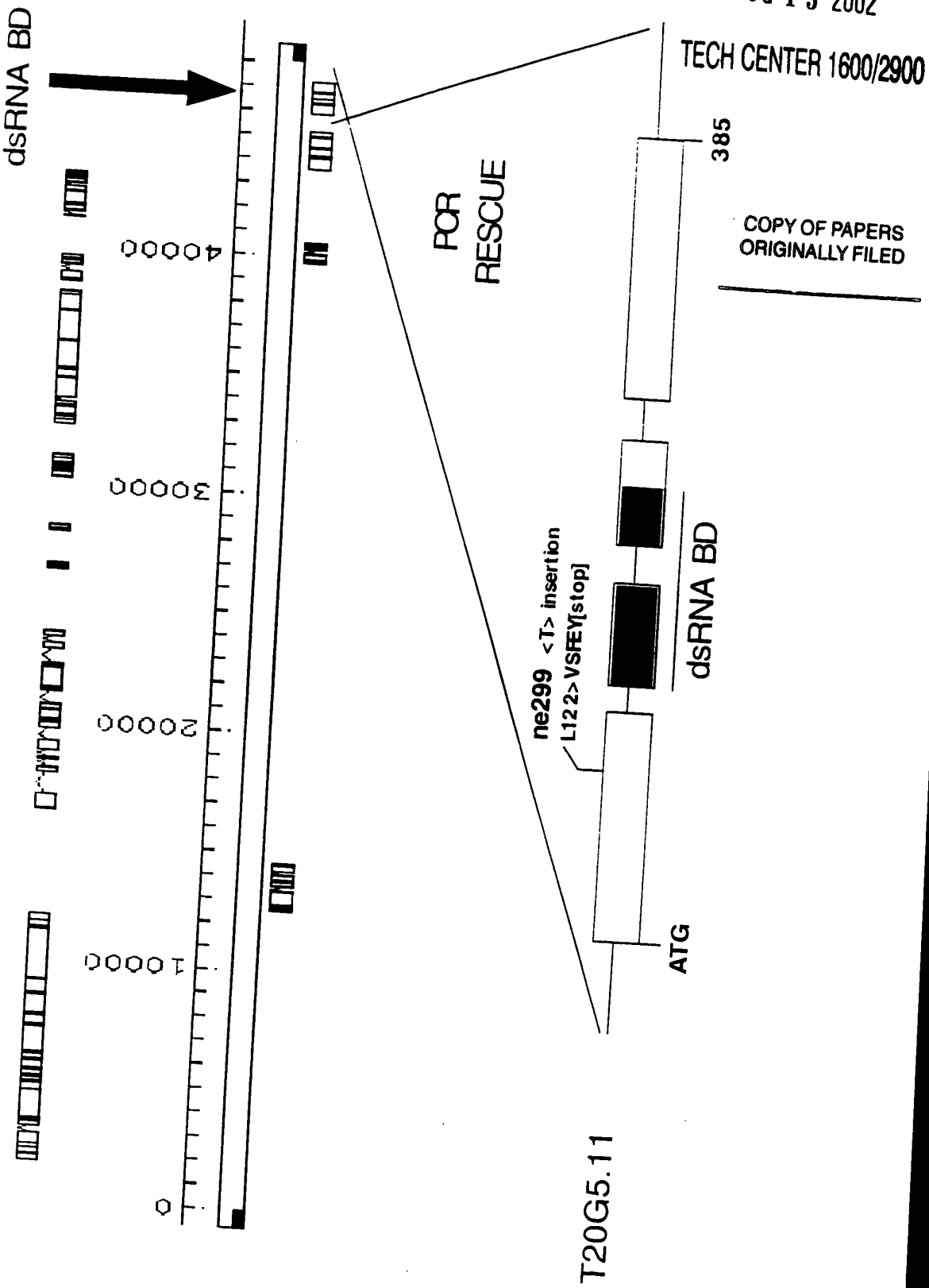

FIG. 12